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1638

TECH CENTER 1600/2900

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/669,476

DATE: 04/05/2001  
 TIME: 08:23:48

Input Set : A:\ES.txt  
 Output Set: N:\CRF3\04052001\I669476.raw

ENTERED

## SEQUENCE LISTING

4 (1) GENERAL INFORMATION:  
 6 (i) APPLICANT: Botella, Jose Ramon  
 8 (ii) TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES  
 10 (iii) NUMBER OF SEQUENCES: 19  
 12 (iv) CORRESPONDENCE ADDRESS:  
 13 (A) ADDRESSEE: MATHEWS, COLLINS, SHEPHERD & GOULD P.A.  
 14 (B) STREET: 100 Thanet Circle, Suite 306  
 15 (C) CITY: Princeton  
 16 (D) STATE: NJ  
 17 (E) COUNTRY: USA  
 18 (F) ZIP: 08540-3662  
 20 (v) COMPUTER READABLE FORM:  
 21 (A) MEDIUM TYPE: Floppy disk  
 22 (B) COMPUTER: IBM PC compatible  
 23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
 26 (vi) CURRENT APPLICATION DATA:  
 C--> 27 (A) APPLICATION NUMBER: US/09/669,476  
 C--> 28 (B) FILING DATE: 25-Sep-2000  
 29 (C) CLASSIFICATION:  
 39 (vii) PRIOR APPLICATION DATA:  
 32 (A) APPLICATION NUMBER: PCT/AU96/00591  
 33 (B) FILING DATE: 20-SEP-1996  
 36 (A) APPLICATION NUMBER: AU PN5559  
 37 (B) FILING DATE: 20-SEP-1995  
 40 (A) APPLICATION NUMBER: AU PN9603  
 41 (B) FILING DATE: 02-MAY-1996  
 43 (viii) ATTORNEY/AGENT INFORMATION:  
 44 (A) NAME: Bernstein, Scott N.  
 45 (B) REGISTRATION NUMBER: 38,827  
 46 (C) REFERENCE/DOCKET NUMBER: 3573-11US  
 48 (ix) TELECOMMUNICATION INFORMATION:  
 49 (A) TELEPHONE: 609-924-8555  
 50 (B) TELEFAX: 609-924-3036  
 53 (2) INFORMATION FOR SEQ ID NO: 1:  
 55 (i) SEQUENCE CHARACTERISTICS:  
 56 (A) LENGTH: 1080 base pairs  
 57 (B) TYPE: nucleic acid  
 58 (C) STRANDEDNESS: single  
 59 (D) TOPOLOGY: linear  
 61 (ii) MOLECULE TYPE: cDNA  
 64 (ix) FEATURE:  
 65 (A) NAME/KEY: CDS  
 66 (B) LOCATION: 1..1080  
 69 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 71 CAG ATG GGG TTT GCG GAG AAC CAG CTT TCG CTG GAG TTA ATA CGT GAG

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72	Gln	Met	Gly	Phe	Ala	Glu	Asn	Gln	Leu	Ser	Leu	Glu	Leu	Ile	Arg	Glu	
73	1				5					10				15			
75	TGG	ATC	AAG	AAT	CAC	CCG	GAG	GCC	TCC	ATT	TGC	TCG	GCG	GAG	GGC	CTG	96
76	Trp	Ile	Lys	Asn	His	Pro	Glu	Ala	Ser	Ile	Cys	Ser	Ala	Glu	Gly	Leu	
77				20					25					30			
79	CCG	CAG	TTC	ATG	GAG	ATC	GCC	AAT	TTC	CAA	GAC	TAC	CAT	GGC	TTG	CCG	144
80	Pro	Gln	Phe	Met	Glu	Ile	Ala	Asn	Phe	Gln	Asp	Tyr	His	Gly	Leu	Pro	
81				35					40					45			
83	GCT	TTT	CTG	CAG	GGA	ATC	GCG	AAA	TTG	ATG	GAG	AAA	GTG	AGA	GGA	GGA	192
84	Ala	Phe	Leu	Gln	Gly	Ile	Ala	Lys	Leu	Met	Glu	Lys	Val	Arg	Gly	Gly	
85		50					55					60					
87	AGG	GTC	AAA	TTC	GAT	CCG	AAC	CGC	GTG	GTG	ATG	AGC	GGC	GGA	GGC	ACT	240
88	Arg	Val	Lys	Phe	Asp	Pro	Asn	Arg	Val	Val	Met	Ser	Gly	Gly	Gly	Thr	
89	65					70					75					80	
91	GGA	GCG	CAA	GAA	ACG	CTC	GCG	TTT	TGT	CTC	GCT	GAC	CCT	GGC	GAC	GCC	288
92	Gly	Ala	Gln	Glu	Thr	Leu	Ala	Phe	Cys	Leu	Ala	Asp	Pro	Gly	Asp	Ala	
93					85					90				95			
95	TTC	CTC	GTC	CCA	ACT	CCG	TAC	TAT	CCA	GCA	TTT	AAT	CGC	GAT	CTC	CGG	336
96	Phe	Leu	Val	Pro	Thr	Pro	Tyr	Tyr	Pro	Ala	Phe	Asn	Arg	Asp	Leu	Arg	
97				100					105				110				
99	TGG	AGA	ACG	GGC	GTC	GAG	CTC	CTC	CCG	GTT	CAC	TGC	AAG	AGC	TCT	AAT	384
100	Trp	Arg	Thr	Gly	Val	Glu	Leu	Leu	Pro	Val	His	Cys	Lys	Ser	Ser	Asn	
101		115						120					125				
103	CAC	TTC	AGA	GTC	ACC	AAA	ACG	GCG	CTA	GAA	TCG	GCA	TAC	GAG	AAG	GCG	432
104	His	Phe	Arg	Val	Thr	Lys	Thr	Ala	Leu	Glu	Ser	Ala	Tyr	Glu	Lys	Ala	
105		130					135					140					
107	CGA	AAG	GAT	AAC	ATC	AGA	GTA	AAA	GGA	GTA	CTG	ATA	ACC	AAC	CCA	TCC	480
108	Arg	Lys	Asp	Asn	Ile	Arg	Val	Lys	Gly	Val	Leu	Ile	Thr	Asn	Pro	Ser	
109	145					150					155				160		
111	AAC	CCG	CTC	GGC	ACG	ACC	ATG	GAT	AAA	CAC	ACG	CTA	CAG	ACC	CTC	GTG	528
112	Asn	Pro	Leu	Gly	Thr	Thr	Met	Asp	Lys	His	Thr	Leu	Gln	Thr	Leu	Val	
113				165					170					175			
115	AAA	TTC	GTA	AAC	GAA	AGG	AGA	ATC	CAC	CTA	GTC	TGC	GAC	GAG	TTA	TAC	576
116	Lys	Phe	Val	Asn	Glu	Arg	Arg	Ile	His	Leu	Val	Cys	Asp	Glu	Leu	Tyr	
117			180					185					190				
119	GGC	GCA	ACC	ATC	TTT	AGG	GAG	CCC	AGG	TTC	GTC	AGC	ATC	TCC	GAG	GTA	624
120	Gly	Ala	Thr	Ile	Phe	Arg	Glu	Pro	Arg	Phe	Val	Ser	Ile	Ser	Glu	Val	
121		195					200					205					
123	ATA	GAA	GAG	GAC	CCG	AAC	TGC	GAC	AAG	AAT	CTG	ATC	CAC	ATT	GCG	TAC	672
124	Ile	Glu	Glu	Asp	Pro	Asn	Cys	Asp	Lys	Asn	Leu	Ile	His	Ile	Ala	Tyr	
125		210				215					220						
127	AGT	CTC	TCA	AAG	GAC	TTC	GGT	CTC	CCC	GGA	TTC	CGA	GTC	GGG	ATC	GTG	720
128	Ser	Leu	Ser	Lys	Asp	Phe	Gly	Leu	Pro	Gly	Phe	Arg	Val	Gly	Ile	Val	
129	225					230					235				240		
131	TAT	TCC	TAC	AAC	GAC	ACG	GTG	GTT	AGT	TGC	GCA	CGC	AGA	ATG	TCG	AGC	768
132	Tyr	Ser	Tyr	Asn	Asp	Thr	Val	Val	Ser	Cys	Ala	Arg	Arg	Met	Ser	Ser	
133				245					250					255			
135	TTC	GGC	CTC	GTC	TCG	TCG	CAG	ACA	CAG	TAC	CTA	CTG	GCC	GCC	ATG	CTA	816
136	Phe	Gly	Leu	Val	Ser	Ser	Gln	Thr	Gln	Tyr	Leu	Leu	Ala	Ala	Met	Leu	

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```

137          260          265          270
139 TCC GGC GAA GAA TTT TTG CCA ACA TTA CTG ACT GAA AGC GCG AAG AGT      864
140 Ser Gly Glu Glu Phe Leu Pro Thr Leu Leu Thr Glu Ser Ala Lys Ser
141          275          280          285
143 CTG TCG GAG AGC CAC AGG ATC TTC TCT TCC GGC CTT GAG GAA GTC GAC      912
144 Leu Ser Glu Ser His Arg Ile Phe Ser Ser Gly Leu Glu Glu Val Asp
145          290          295          300
147 ATC CGC TGC TTG GAC GGC AAT GCC GGG GTC TTC TGC TGG ATG GAC CTA      960
148 Ile Arg Cys Leu Asp Gly Asn Ala Gly Val Phe Cys Trp Met Asp Leu
149 305          310          315          320
151 CGG CAC CTC CTC AAA GAA GCC ACC GAA GAC GGC GAG CTC GAG CTG TGG      1008
152 Arg His Leu Leu Lys Glu Ala Thr Glu Asp Gly Glu Leu Glu Leu Trp
153          325          330          335
155 CGC GTG ATA GTG AAC AAT GTC AAG CTC AAT GTG TCC CCC GGT TCG TCG      1056
156 Arg Val Ile Val Asn Asn Val Lys Leu Asn Val Ser Pro Gly Ser Ser
157          340          345          350
159 TTT TAT TGC GCC GAG CCA GGT TGG      1080
160 Phe Tyr Cys Ala Glu Pro Gly Trp
161          355          360
164 (2) INFORMATION FOR SEQ ID NO: 2:
166 (i) SEQUENCE CHARACTERISTICS:
167 (A) LENGTH: 360 amino acids
168 (B) TYPE: amino acid
169 (D) TOPOLOGY: linear
171 (ii) MOLECULE TYPE: protein
173 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
175 Gln Met Gly Phe Ala Glu Asn Gln Leu Ser Leu Glu Leu Ile Arg Glu
176 1 5 10 15
178 Trp Ile Lys Asn His Pro Glu Ala Ser Ile Cys Ser Ala Glu Gly Leu
179 20 25 30
181 Pro Gln Phe Met Glu Ile Ala Asn Phe Gln Asp Tyr His Gly Leu Pro
182 35 40 45
184 Ala Phe Leu Gln Gly Ile Ala Lys Leu Met Glu Lys Val Arg Gly Gly
185 50 55 60
187 Arg Val Lys Phe Asp Pro Asn Arg Val Val Met Ser Gly Gly Gly Thr
188 65 70 75 80
190 Gly Ala Gln Glu Thr Leu Ala Phe Cys Leu Ala Asp Pro Gly Asp Ala
191 85 90 95
193 Phe Leu Val Pro Thr Pro Tyr Tyr Pro Ala Phe Asn Arg Asp Leu Arg
194 100 105 110
196 Trp Arg Thr Gly Val Glu Leu Leu Pro Val His Cys Lys Ser Ser Asn
197 115 120 125
199 His Phe Arg Val Thr Lys Thr Ala Leu Glu Ser Ala Tyr Glu Lys Ala
200 130 135 140
202 Arg Lys Asp Asn Ile Arg Val Lys Gly Val Leu Ile Thr Asn Pro Ser
203 145 150 155 160
205 Asn Pro Leu Gly Thr Thr Met Asp Lys His Thr Leu Gln Thr Leu Val
206 165 170 175
208 Lys Phe Val Asn Glu Arg Arg Ile His Leu Val Cys Asp Glu Leu Tyr

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```

209          180          185          190
211 Gly Ala Thr Ile Phe Arg Glu Pro Arg Phe Val Ser Ile Ser Glu Val
212          195          200          205
214 Ile Glu Glu Asp Pro Asn Cys Asp Lys Asn Leu Ile His Ile Ala Tyr
215          210          215          220
217 Ser Leu Ser Lys Asp Phe Gly Leu Pro Gly Phe Arg Val Gly Ile Val
218 225          230          235          240
220 Tyr Ser Tyr Asn Asp Thr Val Val Ser Cys Ala Arg Arg Met Ser Ser
221          245          250          255
223 Phe Gly Leu Val Ser Ser Gln Thr Gln Tyr Leu Leu Ala Ala Met Leu
224          260          265          270
226 Ser Gly Glu Glu Phe Leu Pro Thr Leu Leu Thr Glu Ser Ala Lys Ser
227          275          280          285
229 Leu Ser Glu Ser His Arg Ile Phe Ser Ser Gly Leu Glu Glu Val Asp
230          290          295          300
232 Ile Arg Cys Leu Asp Gly Asn Ala Gly Val Phe Cys Trp Met Asp Leu
233 305          310          315          320
235 Arg His Leu Leu Lys Glu Ala Thr Glu Asp Gly Glu Leu Glu Leu Trp
236          325          330          335
238 Arg Val Ile Val Asn Asn Val Lys Leu Asn Val Ser Pro Gly Ser Ser
239          340          345          350
241 Phe Tyr Cys Ala Glu Pro Gly Trp
242          355          360
244 (2) INFORMATION FOR SEQ ID NO: 3:
246 (i) SEQUENCE CHARACTERISTICS:
247 (A) LENGTH: 1104 base pairs
248 (B) TYPE: nucleic acid
249 (C) STRANDEDNESS: single
250 (D) TOPOLOGY: linear
252 (ii) MOLECULE TYPE: cDNA
255 (ix) FEATURE:
256 (A) NAME/KEY: CDS
257 (B) LOCATION: 1..1104
260 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
262 CAG ATG GGC CTT GCT GAG AAT CAG CTT TGC TTT AAT TTA ATT CAC GAG      48
263 Gln Met Gly Leu Ala Glu Asn Gln Leu Cys Phe Asn Leu Ile His Glu
264 1          5          10          15
266 TGG CCG CTG AAA AAC CCA GAA GCC TCC ATT TGT ACA ACA CAA GGA GCA      96
267 Trp Pro Leu Lys Asn Pro Glu Ala Ser Ile Cys Thr Thr Gln Gly Ala
268          20          25          30
270 GCT GAA TTC AGA GAT ATA GCT ATC TTT CAA GAT TAT CAT GGC TTG GCT      144
271 Ala Glu Phe Arg Asp Ile Ala Ile Phe Gln Asp Tyr His Gly Leu Ala
272          35          40          45
274 GAA TTC AGA GAG GCT GTT GCA AAG TTT ATG GGG AAA GTG AGA AGA AAC      192
275 Glu Phe Arg Glu Ala Val Ala Lys Phe Met Gly Lys Val Arg Arg Asn
276          50          55          60
278 AGA GCT TCA TTT GAC CCT GAT CGG ATT GTT ATG AGT GGA GGA GCA ACT      240
279 Arg Ala Ser Phe Asp Pro Asp Arg Ile Val Met Ser Gly Gly Ala Thr
280 65          70          75          80

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282	GGA	GCT	CAT	GAA	ATG	ATT	GGT	TTC	TGT	TTG	GCT	GAT	CCT	GGC	GAT	GCA	288
283	Gly	Ala	His	Glu	Met	Ile	Gly	Phe	Cys	Leu	Ala	Asp	Pro	Gly	Asp	Ala	
284				85					90					95			
286	TTC	TTG	GTT	CCA	ACT	CCT	TAT	TAT	CCA	GGG	TTT	GAT	AGA	GAT	TTG	AGA	336
287	Phe	Leu	Val	Pro	Thr	Pro	Tyr	Tyr	Pro	Gly	Phe	Asp	Arg	Asp	Leu	Arg	
288				100					105					110			
290	TGG	AGA	ACG	GGA	GTC	AAA	CTC	ATT	CCA	GTT	GTC	TGT	GAA	AGC	TCA	AAC	384
291	Trp	Arg	Thr	Gly	Val	Lys	Leu	Ile	Pro	Val	Val	Cys	Glu	Ser	Ser	Asn	
292				115					120					125			
294	GAT	TAC	CAG	ATC	ACC	ATA	GAA	GCC	CTG	GAA	GCT	GCT	TAT	GAA	ACC	GCA	432
295	Asp	Tyr	Gln	Ile	Thr	Ile	Glu	Ala	Leu	Glu	Ala	Ala	Tyr	Glu	Thr	Ala	
296				130					135					140			
298	CAA	GAA	GCT	GAC	ATC	AAG	GTA	AAG	GGT	TTG	GTC	ATA	ACC	AAC	CCA	TCA	480
299	Gln	Glu	Ala	Asp	Ile	Lys	Val	Lys	Gly	Leu	Val	Ile	Thr	Asn	Pro	Ser	
300	145					150						155				160	
302	AAC	CCA	CTG	GGA	ACA	ATT	ATT	ACC	AAG	GAC	ACA	TTA	GAA	GCT	CTA	GTC	528
303	Asn	Pro	Leu	Gly	Thr	Ile	Ile	Thr	Lys	Asp	Thr	Leu	Glu	Ala	Leu	Val	
304						165						170				175	
306	ACC	TTC	ACC	AAC	CAC	AAG	AAC	ATT	CAT	CTG	GTG	TGT	GAT	GAG	ATA	TAT	576
307	Thr	Phe	Thr	Asn	His	Lys	Asn	Ile	His	Leu	Val	Cys	Asp	Glu	Ile	Tyr	
308						180						185				190	
310	GCT	GGT	TAC	CGT	CTT	CAG	CCC	AGG	GCC	GAA	TTC	ACC	AGC	ATA	GCC	GAG	624
311	Ala	Gly	Tyr	Arg	Leu	Gln	Pro	Arg	Ala	Glu	Phe	Thr	Ser	Ile	Ala	Glu	
312									200					205			
314	ATA	ATT	GAA	GAA	GAT	AAA	ATT	TGT	TGC	AAT	CGT	GAT	CTC	ATC	CAC	ATC	672
315	Ile	Ile	Glu	Glu	Asp	Lys	Ile	Cys	Cys	Asn	Arg	Asp	Leu	Ile	His	Ile	
316						210								220			
318	ATT	TAC	AGT	TTA	TCC	AAA	GAC	ATG	GGA	TTC	CCT	GGA	TTT	AGA	GTT	GGC	720
319	Ile	Tyr	Ser	Leu	Ser	Lys	Asp	Met	Gly	Phe	Pro	Gly	Phe	Arg	Val	Gly	
320	225					230						235				240	
322	ATT	GTG	TAT	TCA	TAC	AAT	GAT	GCA	GTG	GTG	AGT	TGT	GCT	CGT	AAG	ATG	768
323	Ile	Val	Tyr	Ser	Tyr	Asn	Asp	Ala	Val	Val	Ser	Cys	Ala	Arg	Lys	Met	
324						245						250				255	
326	TCG	AGC	TTC	GGC	CTA	GTA	TCT	TCG	CAA	ACC	CAG	TAT	CTG	ATT	GCA	TCC	816
327	Ser	Ser	Phe	Gly	Leu	Val	Ser	Ser	Gln	Thr	Gln	Tyr	Leu	Ile	Ala	Ser	
328						260						265				270	
330	ATG	TTA	GCA	GAC	GAT	GAA	TTT	GTA	GAC	AAA	TTT	ATT	GTA	GAG	AGC	AGA	864
331	Met	Leu	Ala	Asp	Asp	Glu	Phe	Val	Asp	Lys	Phe	Ile	Val	Glu	Ser	Arg	
332						275						280				285	
334	AAG	AGG	CTG	GCA	ATG	AGA	CAT	AGT	TTT	TTC	ACA	CAA	AGA	CTT	GCT	CAA	912
335	Lys	Arg	Leu	Ala	Met	Arg	His	Ser	Phe	Phe	Thr	Gln	Arg	Leu	Ala	Gln	
336						290						295				300	
338	GTA	GGC	ATT	AAC	TGT	TTA	AAA	AGC	AAT	GCT	GGT	CTT	TTT	GTG	TGG	ATG	960
339	Val	Gly	Ile	Asn	Cys	Leu	Lys	Ser	Asn	Ala	Gly	Leu	Phe	Val	Trp	Met	
340	305											310				320	
342	GAT	TTG	CGT	AGA	CTG	CTG	AAA	GAA	CAG	ACA	TTT	GAA	GCA	GAA	ATG	GTG	1008
343	Asp	Leu	Arg	Arg	Leu	Leu	Lys	Glu	Gln	Thr	Phe	Glu	Ala	Glu	Met	Val	
344						325						330				335	
346	TTA	TGG	AGA	GTA	ATT	ATA	AAC	GAA	ATG	AAA	CTC	AAT	GTA	TCT	CCT	GGT	1056

VERIFICATION SUMMARY

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L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]